

SEQUENCE LISTING

<110> Jing, Shuqian

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<150> US 60/266,159

<151> 2001-02-02

<150> US 09/723,232

<151> 2000-11-27

<150> US 60/204,208

<151> 2000-05-12

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<170> PatentIn Ver. 2.0

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Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly	Gly	Trp	Leu	Pro	Leu	Leu
			340					345					350		

00840627 034601

Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr  
355 360 365

Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr  
370 375 380

Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile  
385 390 395 400

Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His  
405 410 415

Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala  
420 425 430

Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp  
435 440 445

Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly  
450 455 460

Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu  
465 470 475 480

Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile  
485 490 495

His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys  
500 505 510

Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys  
515 520 525

Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val  
530 535 540

Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu  
545 550 555 560

<210> 6  
<211> 1713  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (273) .. (1427)

<400> 6  
ataaaagcgc agcgtgcggg tggcctggat cccgcgcagt ggcccggcga tgctgctcgt 60  
gctgctaagc ctggccgcgc tgtgcaggag cgccgtaccc cgagagccga ccgttcaatg 120  
tggctctgaa actggggccat ctccagagtg gatgctacaa catgatctaa tcccggggaga 180  
cttgagggac ctccgagtag aacctgttac aactagtgtt gcaacagggg actattcaat 240  
tttgatgaat gtaagctggg tactccgggc ag atg tgg aca ttt tcc tac atc 293  
Met Trp Thr Phe Ser Tyr Ile  
1 5

ggc ttc cct gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat	341
Gly Phe Pro Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn	
10 15 20	
att cct aat gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat	389
Ile Pro Asn Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn	
25 30 35	
ttc acc tca cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag	437
Phe Thr Ser Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys	
40 45 50 55	
tgt gtc aag gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag	485
Cys Val Lys Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys	
60 65 70	
aag aat gag gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga	533
Lys Asn Glu Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly	
75 80 85	
aac aga tac atg gct ctt atc caa cac agc act atc atc ggg ttt tct	581
Asn Arg Tyr Met Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser	
90 95 100	
cag gtg ttt gag cca cac cag aag aaa caa acg cga gct tca gtg gtg	629
Gln Val Phe Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val	
105 110 115	
att cca gtg act ggg gat agt gaa ggt gct acg gtg cag ctg act cca	677
Ile Pro Val Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro	
120 125 130 135	
tat ttt cct act tgt ggc agc gac tgc atc cga cat aaa gga aca gtt	725
Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val	
140 145 150	
gtg ctc tgc cca caa aca ggc gtc cct ttc cct ctg gat aac aac aaa	773
Val Leu Cys Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys	
155 160 165	
agc aag ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct ctg ctg gtg	821
Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val	
170 175 180	
gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg agg cac gaa	869
Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu	
185 190 195	
agg atc aag aag act tcc ttt tct acc acc aca cta ctg ccc ccc att	917
Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile	
200 205 210 215	
aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat cac aca att	965
Lys Val Leu Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile	
220 225 230	
tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc	1013
Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile	
235 240 245	
ctc gaa aag tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag	1061
Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln	
250 255 260	

00840927-034504

tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt 1109  
 Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu  
 265 270 275

tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag 1157  
 Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu  
 280 285 290 295

ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac 1205  
 Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn  
 300 305 310

ctt ttc tgc agt gat cta aga agc cag att cat ctg cac aaa tac gtg 1253  
 Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val  
 315 320 325

gtg gtc tac ttt aga gag att gat aca aaa gac gat tac aat gct ctc 1301  
 Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu  
 330 335 340

agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt 1349  
 Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys  
 345 350 355

gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca 1397  
 Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser  
 360 365 370 375

caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccccaccc atgagaagca 1447  
 Gln Ala Cys His Asp Gly Cys Cys Ser Leu  
 380 385

agagacctta aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg atgatcctga 1507

agcttactat gcagcctaca aacagcctta gtaattaaaa cattttatac caataaaaatt 1567

ttcaaataatt gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc 1627

aaagctgttt tatacataga aatcaattac agctttaatt gaaaactgta accattttga 1687

taatgcaaca ataaagcatc ttcagc 1713

<210> 7

<211> 385

<212> PRT

<213> Homo sapiens

<400> 7

Met Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val  
 1 5 10 15

Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp  
 20 25 30

Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His  
 35 40 45

Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp  
 50 55 60

Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn  
 65 70 75 80

Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His  
85 90 95

Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys  
100 105 110

Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly  
115 120 125

Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys  
130 135 140

Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro  
145 150 155 160

Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu  
165 170 175

Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile  
180 185 190

Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr  
195 200 205

Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu  
210 215 220

Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn  
225 230 235 240

His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile  
245 250 255

Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala  
260 265 270

Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp  
275 280 285

Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp  
290 295 300

Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln  
305 310 315 320

Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr  
325 330 335

Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met  
340 345 350

Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln  
355 360 365

Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser  
370 375 380

Leu  
385

<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
2429-59

<400> 8  
gcagacactg agagcattgt aatcg

25

<210> 9  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
1916-83

<400> 9  
ggctcgtatg ttgtgtggaa ttgtgag

27

<210> 10  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
2429-56

<400> 10  
atcaagaaga cttccttttc tac

23

<210> 11  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer 1916-80

<400> 11  
tgcaaggcga ttaagttggg taacgccag

29

<210> 12  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nested PCR  
Primer

<400> 12  
gccgacgggg acgtggatga ac

22

29

21

28

23

24

[illegible]



Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
20 25 30

[illegible]

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala  
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro  
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr  
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
145 150 155 160

Asp Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
210 215 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
225 230

<210> 22  
<211> 644  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (159)..(641)

<400> 22  
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gaaaataaaaa tcaggactcc taacctgctc cagtcagcct gcttccacga ggccctgtcag 120  
tcagtgcccc acttggtgact gagtgtgcag tgcccagc atg tac cag gtg gtt gca 176  
Met Tyr Gln Val Val Ala  
1 5  
ttc ttg gca atg gtc atg gga acc cac acc tac agc cac tgg ccc agc 224  
Phe Leu Ala Met Val Met Gly Thr His Thr Tyr Ser His Trp Pro Ser  
10 15 20

Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Arg Gly  
100 105 110

Gly

<400> 23															
Met	Ser	Leu	Val	Leu	Leu	Ser	Leu	Ala	Ala	Leu	Cys	Arg	Ser	Ala	Val
1				5					10					15	
Pro	Arg	Glu	Pro	Thr	Val	Gln	Cys	Gly	Ser	Glu	Thr	Gly	Pro	Ser	Pro
			20					25					30		
Glu	Trp	Met	Leu	Gln	His	Asp	Leu	Ile	Pro	Gly	Asp	Leu	Arg	Asp	Leu
		35					40					45			
Arg	Val	Glu	Pro	Val	Thr	Thr	Ser	Val	Ala	Thr	Gly	Asp	Tyr	Ser	Ile
	50					55					60				
Leu	Met	Asn	Val	Ser	Trp	Val	Leu	Arg	Ala	Asp	Ala	Ser	Ile	Arg	Leu
65					70					75					80
Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	Ser
				85					90					95	
Tyr	Ser	Cys	Val	Arg	Cys	Asn	Tyr	Thr	Glu	Ala	Phe	Gln	Thr	Gln	Ser
			100					105					110		
Gly	Gly	Lys	Trp	Thr	Phe	Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn
		115					120					125			
Thr	Val	Tyr	Phe	Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn
	130					135					140				
Glu	Asp	Gly	Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu
145					150					155					160
Asp	His	Ile	Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu
				165					170					175	
Trp	Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu
			180					185					190		
Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile
		195					200					205			
Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln
	210					215					220				
Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser
225					230					235					240

Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser  
245 250 255

Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly  
260 265 270

Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu  
275 280 285

Pro Ala Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro  
290 295 300

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
305 310 315 320

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
325 330 335

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
340 345 350

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
355 360 365

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
370 375 380

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
385 390 395 400

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala  
405 410 415

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
420 425 430

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
435 440 445

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
450 455 460

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
465 470 475 480

Phe Phe Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
485 490 495

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
500 505 510

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
515 520

<210> 25

<211> 585

<212> PRT

<213> Homo sapiens

<400> 24

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val  
1 5 10 15

105160-220180

Pro	Arg	Glu	Pro	Thr	Val	Gln	Cys	Gly	Ser	Glu	Thr	Gly	Pro	Ser	Pro
			20					25					30		
Glu	Trp	Met	Leu	Gln	His	Asp	Leu	Ile	Pro	Gly	Asp	Leu	Arg	Asp	Leu
		35					40					45			
Arg	Val	Glu	Pro	Val	Thr	Thr	Ser	Val	Ala	Thr	Gly	Asp	Tyr	Ser	Ile
	50					55					60				
Leu	Met	Asn	Val	Ser	Trp	Val	Leu	Arg	Ala	Asp	Ala	Ser	Ile	Arg	Leu
	65				70					75					80
Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	Ser
				85					90					95	
Tyr	Ser	Cys	Val	Arg	Leu	Glu	Cys	Ser	Gly	Ala	Ile	Met	Ala	Arg	Cys
			100					105					110		
Asp	Leu	Asn	Leu	Leu	Gly	Ser	Ser	Asp	Arg	Ser	Ala	Ser	Ala	Ser	Arg
		115					120					125			
Ala	Ala	Gly	Thr	Ala	Gly	Val	Gly	His	Gln	Thr	Trp	Leu	Ile	Phe	Val
	130					135					140				
Val	Phe	Val	Glu	Gly	Gly	Phe	Thr	Val	Leu	Leu	Val	Leu	Asn	Ser	Ser
	145				150					155					160
Ala	Gln	Ala	Ile	Cys	Leu	Pro	Arg	Leu	Pro	Lys	Val	Leu	Gly	Leu	Gln
				165					170					175	
Trp	Thr	Phe	Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn	Thr	Val	Tyr
			180					185					190		
Phe	Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn	Glu	Asp	Gly
		195					200					205			
Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu	Asp	His	Ile
		210				215					220				
Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu	Trp	Asp	Pro
	225				230					235					240
Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	Val	Asn	Phe
				245					250					255	
Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile	Gln	His	Ser
			260					265					270		
Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln	Lys	Lys	Gln
		275					280					285			
Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser	Glu	Gly	Ala
	290					295					300				
Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	Thr	Cys	Gly	Ser	Asp	Cys	Ile
	305				310					315					320
Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	Pro	Gln	Thr	Gly	Val	Pro	Phe
				325					330					335	
Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly	Gly	Trp	Leu	Pro	Ala	Ala
			340					345					350		

105420-02460

Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
355 360 365

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
370 375 380

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
385 390 395 400

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
405 410 415

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
420 425 430

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
435 440 445

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
450 455 460

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
465 470 475 480

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
485 490 495

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
500 505 510

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
515 520 525

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
530 535 540

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
545 550 555 560

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
565 570 575

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
580 585

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 26

cattttccta catcggttc cctg

24

<210> 27

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 27  
tgaatctggc ttctttcact gc

22

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008120 22601850